

IN THE DRAWINGS:



Please replace the drawings on file with the replacement drawings submitted herewith. The replacement drawings are submitted to address the Examiner's objections to the drawings and to insert sequence identifiers in Figs. 2 and 3.

REMARKS

The Official Action of March 8, 2005 has been carefully considered and reconsideration of the application as amended is respectfully requested.

Applicants have addressed the objections to the specification appearing at pages 3 and 4 of the Official Actions as follows:

(A) The title of the invention has been amended in the manner courteously suggested by the Examiner;

(B) The specification has been amended to insert a claim to the foreign priority application. (The claim itself was made in the Declaration filed in this matter within the applicable time frame);

(C) The specification has been amended to insert sequence identifiers for the PI-derived and the paleoAP3 motifs, and a revised Sequence Listing has been submitted which encompasses all of the sequences in the application, including the drawings; and

(D) Replacement drawings have been filed which remove the bases for the drawing objections.

The specification has also been amended at page 5, line 11 and page 8, line 14 to correct two (2) clerical errors. The errors and the corrections would have been clear to one of skill in the art from Fig. 3 of the drawing as filed.

With respect to the objection to the claims appearing on page 4 of the Official Action, Applicants respectfully note that the claims have been amended so that they no longer include all nucleic acid molecules that hybridize with the complement strand of the recited nucleic acid molecules, and that the amended claims in fact recite only four (4) nucleotide sequences and degenerate sequences which are patentably indistinguishable from those recited. Applicants respectfully note that the Commissioner has waived the requirements of 37 CFR 1.141 et seq and has directed that fewer than ten (10) separate and distinct nucleotide sequences may be examined in a single application (see MPEP Section 803.04). In view of this directive, Applicants respectfully request the Examiner to permit all of the remaining nucleotide sequences to be claimed in the present application.

The claims have been amended to remove the bases for the rejections under 35 USC 101 and 35 USC 112, second paragraph, appearing at pages 13 and 14 of the Official Action. With particular respect to the amendment to claim 1, it is respectfully noted that a definition of “degeneration sequence” is provided on page 11, lines 26-28 of the specification and that it would have been clear to one of skill in the art from the application as filed that this was meant to refer to the degenerate sequences as now claimed. All claims as amended are respectfully believed to be sufficiently definite to satisfy the dictates of 35 USC 112, second paragraph.

New claims 36-39 have been added more completely to define the subject matter which Applicants regard as their invention.

The claims stand rejected as allegedly failing to comply with the written description requirement of 35 USC 112, first paragraph. The rationale for the rejection appears to relate exclusively to the inclusion in the claims as filed of nucleic acid molecules that hybridize to SEQ ID NO:1. Since the claims have been amended no longer to encompass nucleic acid molecules that hybridize to the complement of the recited nucleic acid molecules, it is respectfully considered that the amendment to the claims has removed the basis for the rejection.

In any event, Applicants respectfully note that, in its Guidelines for Examination of Patent Applications Under the 35 USC 112, paragraph 1 “Written Description” Requirement, 66 Fed. Reg. 1099 (Jan. 5, 2001) (“Guidelines”), the PTO has determined that the written description requirement can be met by “show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics. . .i.e., complete or partial structure, other physical and/or chemical properties, *functional characteristics when coupled with a known or disclosed correlation between function and structure*, or some combination of such characteristics.” Guidelines, 66 Fed. Reg. at 1106 (emphasis added). In the present case, the complete structures of the nucleic acids identified by sequence number have been provided and the degenerate sequences obviously have a known correlation between the recited function (encoding the claimed proteins) and the disclosed structure. Under these circumstances, it is respectfully submitted that all species of nucleic acid within the claimed genus are identified by,

and would be structurally similar to, the species identified by sequence number such that the written description requirement is satisfied (see *Enzo Biochem Inc. v. Gen-Probe Inc.*, 63 USPQ2d 1609, 1615 (Fed. Cir. 2002)). Accordingly, Applicants respectfully request that the rejection on the basis of the written description requirement be withdrawn.

The Examiner has also rejected the claims as allegedly failing to comply with the enablement requirement of 35 USC 112, first paragraph. The rationale for this rejection appears to be that Applicants have failed to provide adequate guidance for how to use the claimed sequence(s), but a utility rejection has not been made under the provisions of 35 USC 101. Under these circumstances, and since the Examiner has recognized that Applicants' specification does in fact teach a number of uses for the claimed nucleic acid molecules (e.g., for comparison of floral morphogenesis and construction of phylogenetic trees), Applicants respectfully question how the 35 USC 112, first paragraph rejection could be applied against the claims directed to the molecules *per se*. See MPEP Section 2164.01(c) ("...when a compound or composition claim is not limited by a recited use, any enabled use that would reasonably correlate with the entire scope of that claim is sufficient to preclude a rejection for nonenablement based on how to use.") Moreover, as discussed next, at the time the present application was filed, the prior art recognized uses for DEF-like MADS-box genes to control floral development, such that a rejection of the claims is respectfully believed to be improper for this reason as well.

With respect to all of the claims, Applicants respectfully note that, for purposes of

enablement, a specification need not disclose what is well-known to those skilled in the art and preferably omits that which is well-known and already available to the public (see MPEP Section 2164.05(a)). In the present case, DEF-like MADS-box genes are well-developed ones for controlling floral development, and there are several successful examples reported for many kinds of plants. Applicant respectfully submit that the guidance of how to use a DEF-like MADS-box gene was well known to persons of ordinary skill of the art at the time the application was filed. The present specification discloses novel MADS-box genes as well as their roles in floral development. Since plant transformation has been well developed, Applicants submit that, with the present disclosure, one of ordinary skill in art could have used, at the time when the invention was made, the DEF-like MADS-box genes to control floral development. In order to support the above statement, the Applicant respectfully call attention to the following references:

(1) Tzeng, T-Y and Yang, C-H. A MADS Box Gene from lily (*Lilium longiflorum*) is Sufficient to Generate Dominant Negative Mutation by Interacting with PISTILLATA (PI) in *Arabidopsis thaliana*. Plant Cell Physiol. 42(10): 1156-1168 (2001): Lily MADS box gene 1 (*LMADS1*) which is derived from lily (*Lilium longiflorum*) is identified as a member of *AP3* family. The *LMADS1* protein was only detected in petals and stamens. Tzeng and Yang constructed an Arabidopsis plants transformed with 35S::*LMADS1*, and found that the transformed plants produced flowers with short petals and stamens. See abstract and Fig. 6.

(2) Krizek, B.A. and Meyerowitz, E.M. The *Arabidopsis* homeotic genes *APETALA3* and *PISTILLATA* are sufficient to provide the B class organ identity function. Development. 122: 11-12 (1996): *APETALA3* and *PISTILLATA* which are derived from *Arabidopsis* are both identified as class B genes. These two genes were required to specify petal and stamen identity in *Arabidopsis* plants. Flowers of plants constitutively expressing both *APETALA3* and *PISTILLATA* under the control of the 35S promoter from cauliflower mosaic virus consist of two outer whorls of petals and inner whorls of stamens. See Abstract and Figs. 1 to 7.

Furthermore, the vector comprising the nucleic acid molecule of the DEF-like MADS-box genes according to the invention is described in the specification on page 12, third paragraph, pages 16 to 17, paragraph "Sequence data analysis" and pages 17 to 18, paragraph "5' rapid amplification of PeMADS cDNA end." Moreover, construction of a vector containing a molecule with a known sequence was also well known to persons skilled in the art. Similarly, as described on pages 12 and 13 of the specification, obtaining a kit comprising the vector and establishing a transformed plant with the vector were also well known to persons skilled in the art.

The Examiner cites Kang (1995, plant Molecular Biology 29(1):1-10) for the proposition that transforming plants with a heterologous rice MADS box gene leads to an unpredictable result. Applicants respectfully submit that the result is not unpredictable. According to the description of the Abstract, OsMADS3 was found to be related with the development of stamen and carpel. The sepals of the transgenic plants that were pale green and

elongated resembled the carpel. Limbs of the corolla of the transgenic plants that were split into sections became antheroid structure tubes attached to tube that resembled filaments (stamen). The altered morphology and coloration of the transgenic plants are all related to the stamen and carpel. The result corresponds to the OsMADS3 function. Given the above, DEF-like MADS-box genes comprising the genes according to the invention and other known genes would be considered to have the ability to control floral development.

The Examiner also contends that B-class gene should specify petal and stamen formation instead of sepal formation. Applicants respectfully refer to the description in page 3, first paragraph of the specification:

"[T]he orchid flower does not have the normal monocots and eudicots floral morphology. It has three sepals, three petals and one of the petals possesses a different morphological structure known as the lip. The male and female reproductive parts are combined in a uniform structure, the column, in the center of the flower. The pollen grains stick together to form pollinia located at the upper end of the column inside the anther (referring to FIG. 1a). As a reason, the result established in the model plant cannot be applied in constructing the mechanism of the elegant orchid floral morphology."

The actual functions of the PeMADS genes are well described on pages 9 to 11 of the specification.

Moreover, Applicants respectfully clarify that obtaining genes controlling floral development by comparison of floral morphogenesis between wild type and peloric mutant is common in this field. Applicants respectfully call attention to the following two documents for the proposition:

(1) Ambrose, B. A. *et al.* Molecular and Genetic Analyses of the *SILKY1* Gene Reveal Conservation in Floral Organ Specification between Eudicots and Monocots. *Molecular Cell*. Vol. 5, 569-579 (2000);

(1) Tsuchimoto S. *et al.* The Whorl-specific action of a petunia class B floral homeotic gene. *Genes to Cells*. Vol. 5, 89-99 (2000).

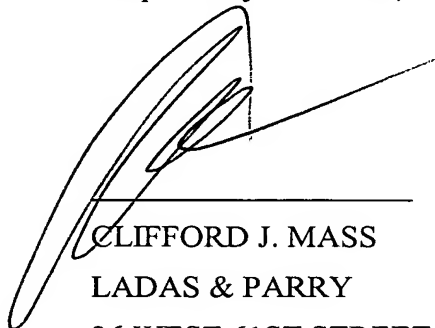
In short, it is respectfully submitted that, based on the guidance in the specification and the knowledge available to those of skill in the art at the time the application was filed, one of skill in the art could have practiced the invention as broadly claimed without undue experimentation. For this reason, it is respectfully requested that the enablement rejection should be withdrawn as to all claims. In any event, the rejection should be withdrawn with respect to the claims to the molecules *per se* for the additional reasons discussed above.

Certain claims stand rejected under 35 USC 102(e) as allegedly being anticipated by Strauss et al, and certain claims stand rejected under 35 USC 102(b) as allegedly being anticipated by Fernandez et al. From the Examiner's comments, it is clear that these rejections were based on the claim recitations which caused the claims to read on all

nucleic acid molecules that hybridize to the complement of SEQ ID NO: 1. These recitations have now been deleted, and the claims no longer read on the molecules described in the cited references. Accordingly, it is respectfully submitted that the prior art rejections of record are not applicable to the amended claims and should be withdrawn.

In view of the above, it is respectfully submitted that all rejections and objections of record have now been overcome and that the application is now in allowable form. An early notice of allowance is earnestly solicited and is believed to be fully warranted.

Respectfully submitted,

A handwritten signature in dark ink, appearing to read 'CLIFFORD J. MASS', is written over a horizontal line. The signature is stylized with a large, sweeping initial 'C'.

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